Amendments to the Claims

This listing of claims will replace all prior versions and listings of all claims in the application.

Claims 1-17 (cancelled)

18. (Previously presented) A method of identifying enzymes with novel catalytic activity, comprising:

a) inputting the three dimensional coordinates of a target protein structure with variable residue positions into a computer;
b) inserting one or more high energy rotamers into said target protein;
c) applying at least one protein design cycle to the target protein structure;
d) generating a set of candidate enzymes with putative catalytic activity;
e) synthesizing a plurality of said candidate enzymes;
f) testing said candidate enzymes for said catalytic activity; and
g) selecting at least one candidate enzyme with catalytic activity.

19. (Previously presented) A method according to claim 18 wherein said active site domain catalyzes a known enzymatic reaction selected from the group consisting of hydrolases, isomerases, transferases, kinases and phosphatases.

20. (Currently Amended) A method according to claim 18 wherein said insertion step is done at the same time as said applying ~~computational~~ step.

21. (Previously presented) A method according to claim 18 further comprising applying a second protein design cycle prior to said generating step.

22. (Currently Amended) A method according to claim 18 in which the protein design cycle comprises PDA ~~protein design automation™~~.

23. (Previously presented) A method according to claim 18 wherein said protein design cycle comprises a DEE computation.

24. (Previously presented) A method according to claim 18 wherein said protein design cycle comprises at least one scoring function.

25. (Previously presented) A method according to claim 24 wherein said scoring function is selected from the group consisting of a van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function.

26. (Previously presented) A method according to claim 18 wherein said protein design cycle comprises a force field calculation.